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The H5N1 virus transmission to human has been observed since 1997, but there has been experience of the subtype N1 at least since 1918. However, scientists showed that the N1 and N2 subtypes could evolve into variants under drug stress. Therefore, our initiative is going to study the impact of point mutation on drug resistance. The goal is to screen a large set of compounds against the same target, the influenza A neuraminidase, with various structures predicted from homology methods thanks to grid infrastructure.

Viral neuraminidase is an enzyme that helps the virus to proliferate and infect more cells, which makes drug resistance a potential concern in case of influenza pandemic. Moreover, the N1 target protein is known to evolve into variants if it comes under drug stress, consequently affecting the efficacy of the present drugs. The idea is to compile the results from in silico screening to know the kinds of compounds and chemical groups (fragments) to be equipped for blocking the active neuraminidases if mutations are to occur at some specific sites. With the help of the high-speed computing and huge data managing capabilities of a grid infrastructure, possible drug components can be screened and studied very rapidly by the available computer modelling application. A grid shares computer power and data storage capacity over the Internet.
During April and may, we have analysed 300,000 possible drug components against 8 different target structures of influenza A neuraminidases using the EGEE (Enabling Grid for E-sciencE), AuverGrid and TWGrid grid infrastructures. About 1500 computers were used during 5 weeks – the equivalent of 100 years on a single computer. More than 60 000 output files with a data volume of 1400 GB were created and stored in a database. Potential drug compounds against avian flu are now being identified and ranked according to the binding energies of the docked models. 1000 of topmost ranked docked complexes will be refined with interaction potential and re-ranked. At least 50 compounds will be assayed experimentally at identified laboratories.

Using the Grid to identify the most promising leads for biological tests could speed up the development process for drugs against the influenza virus. It frees up medicinal chemists' time to better respond to instant, large-scale threats. Moreover, they can concentrate their biological assays in the laboratory on the most promising components, the ones they expect to have the greatest impact.